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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:12:35 ; Search time 42.56 Seconds

(without alignments)
239,268 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343

Sequence: 1 YDIGEELGSGQFAIVKKCRF.....LVKTRKRLTIQELRHPWI 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	83.7	1431	1 DAPK_HUMAN	P53355 homo sapien
2	653.5	48.7	1176	1 KMLS_BOVIN	Q28824 bos taurus
3	647.5	48.2	1906	1 KMLS_CHICK	P11799 gallus gall
4	642.5	47.8	1914	1 KMLS_HUMAN	Q15746 homo sapien
5	639	47.6	397	1 S17A_RABIT	Q99870 oryctolagus
6	638	47.5	414	1 S17A_RABIT	Q99870 oryctolagus
7	636.5	47.4	1147	1 KMLS_HUMAN	Q99870 oryctolagus
8	625	46.5	372	1 S17B_HUMAN	P29294 oryctolagus
9	611.5	45.5	438	1 KMLS_SHEEP	O94768 homo sapien
10	571.5	42.6	607	1 KMLS_SHEEP	O02827 ovie aries
11	570.5	42.5	609	1 KMLS_RABIT	P07313 oryctolagus
12	530.5	39.5	295	1 KMLS_RABIT	P20689 ratuus norv
13	509	37.9	473	1 KMLS_DICDI	P23223-dicystostell
14	506	37.7	474	1 KMLS_HUMAN	Q16566 homo sapien
15	505	37.6	469	1 KMLS_RAT	P13334 ratuus norv
16	500	37.2	3038	1 KCC4_MOUSE	P08414 mus musculu
17	495	36.9	533	1 TRIO_HUMAN	O75962 homo sapien
18	488	36.3	499	1 KCCD_RAT	P15791 ratuus norv
19	485	36.1	370	1 KCCD_HUMAN	Q13557 homo sapien
20	485	36.1	374	1 KCC1_HUMAN	Q14012 homo sapien
21	483.5	36.0	424	1 KPSH_HUMAN	O63450 ratuus norv
22	483	36.0	542	1 KPSH_HUMAN	P18601 homo sapien
23	480	35.7	533	1 CDP3_ORYSA	P53684 oryza sativ
24	479.5	35.7	740	1 CDP2_ORYSA	P53683 oryza sativ
25	478.5	35.6	433	1 DCK1_HUMAN	O13075 homo sapien
26	478.5	35.6	756	1 DCK1_RAT	O08875 ratuus norv
27	475	35.4	478	1 KCCA_RAT	Q91188 mus musculu
28	471	35.1	478	1 KCCA_MOUSE	P11798 mus musculu
29	469	34.9	532	1 KCCG_RAT	P11730 ratuus norv
30	468	34.8	532	1 CDPK_DAUCA	Q28582 daucus caro
31	468	34.8	610	1 CDP1_ARATH	Q06650 arabidopsis
32	464	34.5	534	1 CDP1_ORYSA	P53682 oryza sativ
33	462	34.4	508	1 CDPK_SOYBN	P28583 glycine max

ALIGNMENTS

RESULT	1	STANDARD	PRT	1431 AA.
ID	DAPK_HUMAN			
AC	P53355			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Death-associated protein kinase 1 (EC 2.7.1.1) (DAP kinase 1).			
GN	DAPK1 OR DAPK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95129831; PubMed=7828849;			
RA	Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;			
RT	"Identification of a novel serine/threonine kinase and a novel 15-kD			
RT	protein as potential mediators of the gamma interferon-induced cell			
RT	death.";			
RL	Genes Dev. 9:15-30(1995).			
RN	[2]			
RP	REVISIONS TO 164-171.			
RA	Feinstein E.;			
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL			
CC	DEATH.			
CC	-1- PTM: AUTOPHOSPHORYLATED.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	-1- SIMILARITY: CONTAINS 10 ANK REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	EMBL: X76104; CAA5712.1; ..			
CC	HSSP: O63450; IA06.			
CC	MIM: 600831; ..			
CC	InterPro: IPR002110; ANK.			
CC	InterPro: IPR000488; Death.			
CC	InterPro: IPR002290; Ser_Lhr_PKinase.			
CC	DR Pfam: PF00023; ank. 8.			
CC	DR Pfam: PF00531; death. 1.			
CC	DR Pfam: PF00069; pkinase. 1.			
CC	SMART: SM00248; ANK. 7.			
CC	SMART: SM00005; DEATH. 1.			
CC	SMART: SM00220; S_TKC. 1.			
CC	DR PROSITE: PS50088; ANK_REPEAT. 6.			
CC	DR PROSITE: PS50297; ANK_REPEAT. 1.			
CC	PROSITE: PS50017; DEATH_DOMAIN. 1.			

34	462	34.4	513	1	CDP2_MAIZE	P49101 zea mays (m
35	460	34.3	542	1	KCCB_MOUSE	P28652 mus musculu
36	459	34.2	335	1	KCC1_SCHPO	Q9P712 schizosacch
37	458	34.1	512	1	KI10_ARATH	Q38997 arabidopsis
38	457	34.0	542	1	KCCB_RAT	P08413 ratuus norv
39	457	34.0	664	1	KCCB_HUMAN	O13554 homo sapien
40	456.5	34.0	406	1	KPBH_RAT	P1335 ratuus norv
41	452.5	33.7	406	1	KPBH_HUMAN	P15735 homo sapien
42	452	33.7	386	1	KPB6_RABIT	P00518 oryctolagus
43	450	33.5	909	1	CSKP_RAT	Q62915 ratuus norv
44	450	33.5	921	1	CSKP_HUMAN	O14936 homo sapien
45	450	33.5	924	1	CSKP_MOUSE	O70589 mus musculu

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KM Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
 FT DOMAIN 13 266 CALMODULIN-BINDING.
 FT REPEAT 267 334
 FT REPEAT 378 407 ANK 1.
 FT REPEAT 411 440 ANK 2.
 FT REPEAT 444 473 ANK 3.
 FT REPEAT 478 507 ANK 4.
 FT REPEAT 511 540 ANK 5.
 FT REPEAT 544 573 ANK 6.
 FT REPEAT 577 606 ANK 7.
 FT REPEAT 610 639 ANK 8.
 FT REPEAT 876 905 ANK 9.
 FT REPEAT 1163 1197 ANK 10.
 FT REPEAT 1313 1397 DEATH.
 FT NP_BIND 19 27 ATP (BY SIMILARITY).
 FT BINDING 42 42 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MOTIFGEN 42 42 K->A: LOSS OF ACTIVITY.
 FT SEQUENCE 1431 AA; 160017 MW; 9EB84611004A155B CRC64;

Query Match 83.7%; Score 1124; DB 1; Length 1431;
 Best Local Similarity 79.5%; Pred. No. 5,8e-65;
 Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

OY 1 YDIGEELSGGQFAIVYKKREKSTGLVAAKFKKRSRSGVSRREIEEVSILRQVL 60
 DB 13 YDIGEELSGGQFAIVYKKREKSTGLVAAKFKKRSRSGVSRREIEEVSILRQVL 72
 OY 61 HHNVITLHDVYENRIVHILEVSGSELDFLAOKESISEEARSFKQILIDGVNYVHT 120
 DB 73 HHNVITLHDVYENRIVHILEVSGSELDFLAOKESISEEARSFKQILIDGVNYVHT 132
 OY 121 KKAHPDLAKENIMLDKNIPRIHKLIDGLAHEIDGVEFKNIETGEFVAPRIYVNE 180
 DB 133 LQIAHPDLAKENIMLDKNIPRIHKLIDGLAHEIDGVEFKNIETGEFVAPRIYVNE 192
 OY 181 PLGLEADMSIGVITYITLLSGASPFGLDTRKQETLANITSVSDPEDEFFSHSELAKDFI 240
 DB 193 PLGLEADMSIGVITYITLLSGASPFGLDTRKQETLANITSVSDPEDEFFSHSELAKDFI 252
 OY 241 RLLVKEETRRKRLTQELRHPWI 263
 DB 253 RLLVKEETRRKRLTQELRHPWI 275
 RESULT 2
 ID KMLS_BOVIN STANDARD; PRT; 1176 AA.
 AC Q28824;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MCK)
 DE [contains: Telokin].
 GN MYLK.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RX MEDLINE=93203148; PubMed=1284247;
 RA Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T.,
 Ebashi S.;
 RT "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
 myosin light chain kinase activity.";

RL J. Biochem. 112:786-791(1992).
 CC -1- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
 CC SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
 CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
 CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] -> ADP + [myosin
 CC light-chain] phosphate.
 CC -1- SUBUNIT: TELOKIN BINDS CALMODULIN.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS OF MCK ARE PRODUCED BY
 CC ALTERNATIVE INITIATION, A NON-MUSCLE FORM (WHICH IS THE LONGEST
 CC FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
 CC NO CATALYTIC ACTIVITY). THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: BELONGS TO IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: S57131; AAB25794.1; -.
 DR HSSP; P56276; ITRK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003598; Iq_C2.
 DR InterPro: IPR003600; Iq_Like.
 DR InterPro: IPR002280; Ser_thr_pkinase.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Iq; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00410; Iq_Like; 1.
 DR SMART; SM00408; IqC2; 2.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
 DR Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
 KW Alternative Initiation.
 FT CHAIN 1 1176
 FT INIT_MET 1022 1176
 FT DOMAIN 100 291
 FT REPEAT 100 111
 FT REPEAT 112 123
 FT REPEAT 124 135
 FT REPEAT 136 147
 FT REPEAT 148 159
 FT REPEAT 160 171
 FT REPEAT 172 183
 FT REPEAT 184 195
 FT REPEAT 196 207
 FT REPEAT 208 219
 FT REPEAT 220 231
 FT REPEAT 232 243
 FT REPEAT 244 255
 FT REPEAT 256 267
 FT REPEAT 268 279
 FT REPEAT 280 291
 FT DOMAIN 603 673
 FT DOMAIN 673 725
 FT DOMAIN 725 792
 FT DOMAIN 792 1035
 FT NP_BIND 1084 1151
 FT NP_BIND 731 739
 FT BINDING 754 754
 FT ACT_SITE 846 846
 MYOSIN LIGHT CHAIN KINASE. SMOOTH-MUSCLE
 ISOZYME.
 TELOKIN.
 FOR TELOKIN.
 16 X 12 AA TANDEM REPEATS.
 1.
 2.
 3 (INCOMPLETE).
 4.
 5.
 6.
 7.
 8.
 9.
 10.
 11.
 12.
 13.
 14.
 15.
 16.
 FIBRONECTIN TYPE-III.
 PROTEIN KINASE.
 CALMODULIN-BINDING.
 IG-LIKE C2-TYPE DOMAIN.
 ATP (BY SIMILARITY).
 ATP (BY SIMILARITY).
 BY SIMILARITY.

FT DOMAIN 1171 1176 POLY-GLU.
SQ SEQUENCE 1176 AA: 128824 MW: F53DC6D4D42D4B97 CRC64;
Query Match 48.7%; Score 653.5; DB 1; Length 1176;
Best Local Similarity 48.5%; Pred. No. 7.8e-35;
Matches 128; Conservative 48; Mismatches 79; Indels 9; Gaps 3;
OY 1 YDGEELSGOFAIVKCKREKSGLEYAKFKIKKRSRARSRRVSREREYSILROVL 60
DB YDIEELRSGSKFGVFLVKEGKTKWAGKFKAYSAR-----EKENINQEIISINMCLH 778
OY 61 HHNVITLHDVYENRTDVNHLIELVSGELPDLFAOKE-SLSEEPATSEIKQIDGVNYLH 119
DB HPLVOCVDAFEERKANIVWLVEIVSGELFERIIDEFELTEBCEIKYMKQISEGYEYIH 838
OY 120 TKKIAHFDLKPENIMLLDKNIPPIKRLIDGLAHEIDGVEERKNIFGPPEVAPELIVNY 179
DB KQGIIVHLDLKPEINIMCVNKT--GTRIKLIDFGLARLENAGSLKVLFGPPEVAPEVINY 896
OY 180 EPLGLADWMSIGVITYIILLSGASPLGDTKQETLANITSVSDPDEEFSSHSLAKDF 239
DB EPLGVATDMWSIGVICYILLVSGLSPPMGDNDNETLANVTSATWDFDEAFDEISDAKDF 956
OY 240 IRKLAVETRRKRLTIOEALRPMI 263
DB 957 ISMLKKDKMKNRKNCQCLQHPWL 980
RESULT 3
KMLS-CHICK STANDARD; PRT: 1906 AA.
ID P1179: P19038:
AC 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase, smooth muscle and non-muscle isozymes
DE (EC 2.7.1.117) (MCKK) [contains: Telokin].
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (MCKK-210).
RX MEDLINE=96033976; PubMed=7589469;
RA Waterson D.M., Collinge M., Lukas T.J., van Eldik L.J., Birukov K.G.,
RA Stepanova O.V., Shtrinsky V.P.;
RT "Multiple gene products are produced from a novel protein kinase
RT transcription region.";
RL FEBS Lett. 373:217-220(1995).
RN [2]
RP SEQUENCE FROM N.A. (MCKK-108).
RX MEDLINE=90192792; PubMed=2315380;
RA Olson N.J., Pearson R.B., Needleman D.S., Hurwitz M.J., Kemp B.E.,
RA Means A.R.;
RT "Regulatory and structural motifs of chicken gizzard myosin light
RT chain kinase.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).
RN [3]
RP SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=90361738; PubMed=2202734;
RA Shoemaker M.O., Lau W., Shattuck R.L., Klatkowski A.P.,
RA Matristian P.E., Guerra-Santos L., Wilson E., Lukas T.J.,
RA van Eldik L.J., Waterson D.M.;
RT "Use of DNA sequence and mutant analyses and antisense
RT oligodeoxynucleotides to examine the molecular basis of nonmuscle
RT myosin light chain kinase autoinhibition, calmodulin recognition, and
RT activity.";
RL J. Cell Biol. 111:1107-1125(1990).
RN [4]
RP SEQUENCE OF 1259-1906 FROM N.A.

RC TISSUE=gizzard;
RX MEDLINE=87157587; PubMed=3030394;
RA Guerriero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Means A.R.;
RT "Domain organization of chicken gizzard myosin light chain kinase
RT deduced from a cloned cDNA.";
RL Biochemistry 25:8372-8381(1986).
RN [5]
RP SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
RC TISSUE=gizzard;
RX MEDLINE=93073972; PubMed=1444462;
RA Yoshikai S., Ikebe M.;
RT "Molecular cloning of the chicken gizzard telokin gene and cDNA.";
RL Arch. Biochem. Biophys. 299:242-247(1992).
RN [6]
RP SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN).
RX MEDLINE=92326611; PubMed=1373815;
RA Collinge M., Matristian P.E., Zimmer W.E., Shattuck R.L., Lukas T.J.,
RA van Eldik L.J., Waterson D.M.;
RT "Structure and expression of a calcium-binding protein gene contained
RT within a calmodulin-regulated protein kinase gene.";
RL Mol. Cell. Biol. 12:2359-2371(1992).
CC - FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/
CC MCKK SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE
CC TRANSDUCTION OF CALCIUM SIGNALS.
CC - CATALYTIC ACTIVITY: ATP + [myosin light-chain] - ADP + [myosin
CC light-chain] phosphate.
CC - ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS OF MCKK ARE PRODUCED
CC BY ALTERNATIVE INITIATION, A NON-MUSCLE FORM (MCKK-210), WHICH IS
CC THE LONGEST FORM; A SMOOTH-MUSCLE FORM (MCKK-108) AND TELOKIN (A
CC C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).
CC - TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN GIZZARD, HEART, LUNG,
CC INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE
CC EXPRESSION IN THE LATTER WERE MUCH LESS THAN THAT IN THE GIZZARD.
CC - DOMAIN: TELOKIN BINDS CALMODULIN.
CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC - SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC
CC EMBL: X52876; CAA37056.1; -
CC EMBL: X52876; CAA37057.1; -
CC EMBL: X52876; CAA37058.1; -
CC EMBL: M31048; AAA49069.1; -
CC EMBL: M14953; AAA68964.1; -
CC EMBL: M96655; AAA49083.1; -
CC EMBL: M88283; AAA48647.1; -
CC EMBL: M88284; AAB53768.1; -
CC PIR: A25810; A25810.
CC PIR: A37099; A37099.
CC PIR: S11652; S11652.
CC HSSP: P56276; ITLK.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR003600; Ig_Like.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00047; Ig_9.
CC Pfam: PF00069; pkinase.1.
CC SMART: SM00060; FN3; 1.
CC SMART: SM00410; Ig_Like; 1.
CC SMART: SM00408; IgC2; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_SF: 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM: 1.
 DR Transferrase: Serine/threonine-protein kinase: Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
 KW Alternative Initiation.
 FT CHAIN 1 1906
 FT CHAIN 935 1906
 FT CHAIN 1750 1906
 FT INT_MET 935 1906
 FT INT_MET 1750 1906
 FT DOMAIN 1750 1906
 FT DOMAIN 1330 1400
 FT DOMAIN 1453 1708
 FT DOMAIN 1809 1876
 FT NP_BIND 1459 1467
 FT BINDING 1482 1482
 FT ACT_SITE 1574 1574
 FT DOMAIN 1716 1728
 FT DOMAIN 1730 1749
 FT DOMAIN 1317 1364
 FT DOMAIN 1385 1402
 FT DOMAIN 660 1833
 FT REPEAT 660 676
 FT REPEAT 758 774
 FT REPEAT 1107 1123
 FT REPEAT 1817 1833
 FT REPEAT 683 1866
 FT DOMAIN 693 708
 FT REPEAT 807 807
 FT REPEAT 791 807
 FT REPEAT 1140 1156
 FT REPEAT 1281 1297
 FT REPEAT 1851 1866
 FT DOMAIN 970 1226
 FT REPEAT 970 987
 FT REPEAT 999 1016
 FT REPEAT 1061 1078
 FT REPEAT 1209 1226
 FT DOMAIN 1700 1763
 FT DOMAIN 1896 1906
 FT MOD_RES 1748 1748
 FT MOD_RES 1762 1762
 FT CONFLICT 1439 1439
 FT CONFLICT 1906 AA; 210445 MW; AD7D8A3B69EE3363 CRC64;
 SQ SEQUENCE

Query Match 48.28; Score 647.5; DB 1; Length 1906;
 Best Local Similarity 48.14; Pred. No. 3.3e-34;
 Matches 127; Conservative 48; Mismatches 80; Indels 9; Gaps 3;

1 YDIGELGGGFAIVKCKREKSTGLEAAFKIKKRSRRASRGVSREETREVSILROYL 60
 1453 YNTERLSSGRFGVFLVEKKTGKVNAGKFKAYSAK-----EKENIDETISNMCULH 1506
 61 HHNVITLHDVYENRTDVHIELVSGELFPLAOKS-SISEBATSEFIQIIDGVNYTH 119
 1507 HKPLVOCVDAPEEKANIYVLEWVSGELFERIIDDEPTELCITVMKQISGAYTII 1566
 120 TKKIHFDLKPENIMLLDKNIPPIKILIDFLAHEIDEGVEFNKIFGTPEFAVELVNY 179
 1567 KGIYHLDLKPENIMCVNKT--GTSIKILIDFLGRLARLESAGSLVLFOTPEFAVEVINY 1624
 180 EPLGLEADMSIGVITYILLGASPLDQKQETLANITSYDPDEFESHTSEILAKDF 239
 1625 EPKIGVETDMSIGVICYIIVSGLSPMGNDNETLANVTSATWDFDEAFDEISDDAKDF 1664
 240 IRKLVLKRETRKRLTIOEALRHPWI 263
 1685 ISMLKKDKMSRLNCTQCLOHPWL 1708

RESULT 4
 KMLS_HUMAN STANDARD: PRT: 1914 AA.
 ID KMLS_HUMAN
 AC Q15746; Q14844; Q16794; Q95796; Q95797; Q95798; Q95799; Q9UBG5;
 AC Q9UTR9;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase, smooth muscle and non-muscle isoforms
 DE (EC 2.7.1.117) (MLCK) [Contains: Telokin (kinase related protein)
 DE (KRP)].
 GN MYLK OR MLCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1);
 RP TISSUE=umbilical vein endothelial cells;
 RP MEDLINE=97304466; PubMed=9160829;
 RA Garcia J.G.N., Lazar V.L., Gilbert-McClain L.I., Gallagher P.J.,
 RA Verin A.D.;
 RA "Myosin light chain kinase in endothelium: molecular cloning and
 RA regulation";
 RA Am. J. Respir. Cell Mol. Biol. 16:489-494(1997).
 RN [2]
 RP REVISIONS.
 RP Blukov K.G., Garcia J.G.N.;
 RP Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2; 3A; 3B AND 4).
 RP TISSUE=umbilical vein;
 RP MEDLINE=99216419; PubMed=10198165;
 RA Lazar V.L., Garcia J.G.N.;
 RA "A single human myosin light chain kinase gene (MLCK; MYLK).";
 RA Genomics 57:256-267(1999).
 RN [4]
 RP REVISIONS TO ISOFORM 2.
 RP Blukov K.G., Garcia J.G.N.;
 RP Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 923-1914 FROM N.A.
 RP TISSUE=Hippocampus;
 RP MEDLINE=96121365; PubMed=8575746;
 RA Potier M.-C., Chelot E., Pekarsky Y., Gardiner K., Rossier J.,
 RA Turnell W.G.;
 RA "The human myosin light chain kinase (MLCK) from hippocampus:
 RA cloning, sequencing, expression, and localization to 3qcen-q21";
 RA Genomics 29:562-570(1995).
 RN [6]
 RP SEQUENCE OF 1614-1914 FROM N.A.
 RP TISSUE=Lung, and Placenta;
 RP MEDLINE=20007838; PubMed=10536370;
 RA Waterson D.M., Schavocky J.P., Guo L., Weiss C., Chlenski A.,
 RA Shlinsky V.P., Van Eldik L.J., Halech J.;
 RA "Analysis of the kinase-related protein gene found at human chromosome
 RA 3q21 in a multi-gene cluster: organization, expression, alternative
 RA splicing and polymorphic marker";
 RA J. Cell. Biochem. 75:461-491(1999).
 RN [7]
 RP SEQUENCE OF 1456-1914 FROM N.A.
 RP TISSUE=Placenta;
 RA Waterson M.D.;
 RA Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
 CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC). AN EVENT THAT
 CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL
 CC DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE
 CC EDEMA FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO
 CC CONTROL THE GROWTH INITIATION OF ASTROCYTIC PROCESSES IN CULTURE
 CC AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED
 CC BETWEEN CULTURED SYMPATHETIC GANGLION CELLS. CRITICAL PARTICIPANT

CC		IN SIGNALING SEQUENCES THAT RESULT IN FIBROBLAST APOPTOSIS.
CC	-I-	CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC		light-chain] phosphate.
CC	-I-	SUBUNIT: TELOKIN BINDS CALMODULIN.
CC	-I-	ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A NON-MUSCLE FORM (THE
CC		LONGEST FORM), A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL
CC		SECTION WITH NO CATALYTIC ACTIVITY); ARE PRODUCED BY ALTERNATIVE
CC		INITIATION.
CC	-I-	ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; 1 (SHOWN HERE), 2, 3A,
CC		3B, 4 AND DEL-1790; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-I-	TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE
CC		EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN
CC		CULTURED ENDOTHELIAL WITH QUALITATIVE EXPRESSION APPEARING TO BE
CC		NEITHER TISSUE-NOR DEVELOPMENT-SPECIFIC. NON-MUSCLE ISOFORM 2 IS
CC		THE DOMINANT SPICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN
CC		HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
CC	-I-	PWM: MLCk IS PROBABLY DOWN-REGULATED BY PHOSPHORYLATION.
CC	-I-	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	-I-	SIMILARITY: CONTAINS 1 IMMUGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	-I-	SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way
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CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC		or send an email to license@isb-sib.ch).
CC		-----
DR	EMBL:	U48959; AAC18423.2; -
DR	EMBL:	AF0695601; AAD15921.2; -
DR	EMBL:	AF0695602; AAD15922.1; -
DR	EMBL:	AF0695603; AAD15923.1; -
DR	EMBL:	AF0695604; AAD15924.1; -
DR	EMBL:	X85337; CAAS9685.1; -
DR	EMBL:	AF096771; AADS1380.1; -
DR	EMBL:	AF096766; AAD51380.1; JOINED.
DR	EMBL:	AF096767; AAD51380.1; JOINED.
DR	EMBL:	AF096768; AAD51380.1; JOINED.
DR	EMBL:	AF096769; AAD51380.1; JOINED.
DR	EMBL:	AF096770; AAD51380.1; JOINED.
DR	EMBL:	AF096774; AADS4018.1; -
DR	EMBL:	AF096771; AAD51381.1; -
DR	EMBL:	AF096769; AAD51381.1; JOINED.
DR	EMBL:	AF096770; AAD51381.1; JOINED.
DR	EMBL:	X90870; CAAG2378.1; -
DR	HSSP:	P56276; ITKL.
DR	MIM:	600922; -
DR	InterPro:	IPR000719; Euk_Pkinase.
DR	InterPro:	IPR003961; FN_III.
DR	InterPro:	IPR003962; FNIII_repeat.
DR	InterPro:	IPR003006; Ig_MHC.
DR	InterPro:	IPR003598; Ig_C2.
DR	InterPro:	IPR003600; Ig_Like.
DR	InterPro:	IPR002290; Ser_thr_kinase.
DR	Pfam:	PF00041; fn3.1.
DR	Pfam:	PF00047; Ig.8.
DR	Pfam:	PF00063; Pkinase.1.
DR	PRINTS:	PR00014; ENTPEPITI.
DR	SMART:	SMO0060; FN3.1.
DR	SMART:	SMO0410; IG_Like.1.
DR	SMART:	SMO0408; IGC2.8.
DR	SMART:	SMO0220; S_TKC.1.
DR	PROSITE:	PS00107; PROTEIN_KINASE_ATP.1.
DR	PROSITE:	PS00108; PROTEIN_KINASE_ST.1.
DR	PROSITE:	PS50011; PROTEIN_KINASE_DOM.1.
KW	Transferrase;	Serine/threonine-protein kinase; Calmodulin-binding;
KW	ATP-binding;	Phosphorylation; Immunoglobulin domain; Repeat;
KW	Alternative initiation;	Alternative splicing.
FT	CHAIN	1 1914
FT		ISOYME.
FT		MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT		ISOYME.
FT		MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT		ISOYME.
FT	CHAIN	923 1914
FT		ISOYME.
FT		MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT		ISOYME.

FT	CHAIN	1761	1914		TELOKTIN.
FT	INIT_MET	923	923		FOR MOSIN LIGHT CHAIN KINASE, SMOOTH-
FT	INIT_MET				MUSCLE ISOZYME.
FT	INIT_MET	1761	1761		FOR TELOKIN.
FT	DOMAIN	1343	1413		FIBROECTIN TYPE-III.
FT	DOMAIN	1464	1719		CALMODULIN-BINDING.
FT	DOMAIN	1711	1774		IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	1824	1891		AAP (BY SIMILARITY).
FT	NP_BIND	1470	1478		AAP (BY SIMILARITY).
FT	BINDING	1493	1493		BY SIMILARITY.
FT	ACT_SITE	1585	1585		POLY-GLU.
FT	DOMAIN	1906	1914		5 X 28 AA APPROXIMATE TANDEM REPEATS.
FT	DOMAIN	868	998		I-1.
FT	REPEAT	868	895		I-2.
FT	REPEAT	896	923		I-3.
FT	REPEAT	924	951		I-4.
FT	REPEAT	952	979		I-5 (INCOMPLETE).
FT	REPEAT	980	968		G 12 AA APPROXIMATE TANDEM REPEATS.
FT	DOMAIN	999	1063		I-1 (INCOMPLETE).
FT	REPEAT	999	1003		I-2.
FT	REPEAT	1004	1015		I-3.
FT	REPEAT	1016	1027		I-4.
FT	REPEAT	1028	1039		I-5.
FT	REPEAT	1040	1051		I-6.
FT	REPEAT	1052	1063		VSDISPEVAMELEGTVPVRROEGSIIEVDAGSHYLCLKRK
FT	VARSPPLIC	437	506		RTRDSCTSGTASNNAGOVSCSWTLQVER -> G (IN
FT	VARSPPLIC				ISOFORM 2 AND ISOFORM 3B).
FT	VARSPPLIC	1433	1439		DEVEDND -> MKMRCOP (IN ISOFORM 3A,
FT	VARSPPLIC				ISOFORM 3B AND ISOFORM 4).
FT	VARSPPLIC	1473	1546		NCHHPRKLVCVDAFEAKRKNWAGFFFKVAISKERENIROEISIIM
FT	VARSPPLIC				(IN ISOFORM 4).
FT	VARSPPLIC	1655	1705		MISSING (IN ISOFORM 3A AND ISOFORM 3B).
FT	VARSPPLIC	1790	1790		MISSING (IN ISOFORM DEL-1790).
FT	CONFLICT	933	933		V -> M (IN REF. 5).
FT	CONFLICT	963	963		S -> P (IN REF. 3); AAD15922).
FT	CONFLICT	1022	1022		P -> A (IN REF. 5).
FT	CONFLICT	1048	1050		KPM -> EAH (IN REF. 5).
FT	CONFLICT	1162	1162		P -> L (IN REF. 3; AAD15922 AND
FT	CONFLICT				AAD15923).
FT	CONFLICT	1210	1210		L -> P (IN REF. 5).
FT	CONFLICT	1280	1280		E -> D (IN REF. 3; AAD15922 AND
FT	CONFLICT				AAD15923).
FT	CONFLICT	1284	1284		M -> I (IN REF. 3; AAD15922, AAD15923 AND
FT	CONFLICT				AAD15924).
FT	CONFLICT	1300	1300		A -> G (IN REF. 5).
FT	CONFLICT	1316	1316		L -> S (IN REF. 5).
FT	CONFLICT	1326	1326		T -> S (IN REF. 5).
FT	CONFLICT	1478	1478		V -> C (IN REF. 5).
FT	CONFLICT	1511	1511		S -> T (IN REF. 3; AAD15922 AND
FT	CONFLICT				AAD15923).
FT	CONFLICT	1563	1563		I -> T (IN REF. 5).
FT	CONFLICT	1609	1609		A -> P (IN REF. 5).
FT	CONFLICT	1639	1639		G -> R (IN REF. 5).
FT	CONFLICT	1640			GY -> D (IN REF. 3; AAD15922, AAD15923
Query Match		47.88;			Score 642.5; DB 1; Length 1914;
Best Local Similarity		47.7%;			Pred. No. 6; 8e-34;
Matches 126; Conservative		49;			Mismatches 80; Indels 9; Gaps
Oy	1 YDIGELGSGGFAYVKCKCRKSSTGLVEAAAFIKKKRSRASRGVSNEEREVESTLRQVL 60				
Db	1464 YIDIERLSSGGFGGVFLPVEKTKRWKAFFFAYSAK-----EEENIRKIISTMNCLH 1517				
Oy	61 HANVTLLHDVVENRTDVVHLIELVSGSELDPDLPAQKE-SISEBEATSFIFQLDGVNVLH 119				
Db	1518 HPRLVGCVDADEEKANKNTVMLEIVSGSELPFRITDDFELTREBCIKMKWRJSEGEVIH 1577				
Oy	120 TKRAHAEDPKPENMLDKNIPIPHIKLIDGLAHEIEDGVEEKNI FGTPEVVAPEIYN 179				
Db	1578 KGAIYHLDLKPEENIMCVNK--GTRIKLIIDGLCARLRLENAGSLKYLVGTPEVVAPEIYN 1635				

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OY 180 EPLGLDMSIGVITVILLGSGAPLGDQKQETLANITSVSDPEEFHSHTSELANOF 239
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1636 EPIYATDMSIGVICYIIVSGLSFPGDNDNETLANVTSATWDFDEAFDEISDADKF 1695
OY 240 IRLKLVETRRKRLTIQALRHPMI 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1696 ISNLKDKMKRNLDCCTCLQHPWL 1719

RESULT 5
S17A_RABIT STANDARD; PRT; 397 AA.
ID S17A_RABIT
AC 09670: 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related
apoptosis-inducing protein kinase 1) (rDRAK1).
GN STK17A OR DRAK1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=osteoclast;
RX MEDLINE=2176420; PubMed=11279167;
RA Kojima H., Nemoto A., Uemura T., Honma R., Ogunu M., Liu Y.-K.;
RA "DRAK1, a novel kinase related to apoptosis, is strongly expressed in
active osteoclasts and induces apoptosis."
RT J. Biol. Chem. 276:19238-19243(2001)
CC -1- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) (BY
SIMILARITY) AND IS INVOLVED IN OSTEOCLAST APOPTOSIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BONE MARROW AND IN LOWER
LEVELS IN BRAIN, HEART, LUNG, LIVER AND KIDNEY.
CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
DR EMBL; AB042195; BAB1611.1; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Nuclear protein; Apoptosis.
FT DOMAIN 44 304 PROTEIN KINASE.
FT NP_BIND 50 58 ATP (BY SIMILARITY).
FT BINDING 73 73 ATP (BY SIMILARITY).
SQ SEQUENCE 397 AA; 44462 MW; 569041E107F50097 CRC64;

Query Match 47.6%; Score 639; DB 1; Length 397;
Best Local Similarity 46.0%; Pred. NO. 2e-34;
Matches 122; Conservative 64; Mismatches 67; Indels 12; Gaps 6;
OY 4 GEEIGSGQFAIVKCRKSTGLEAYAKFKKQSRASRGVS-REIEREVSILQVJHH 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 GREIGRGKFAVVRKCIQKDSGEFAKFKRRK-----RKGDCCRMELIHEIIVL-ELAD 100

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OY 63 N-VITLHDYENKRTDVHILVELSGGLFD--FLAKRESLSEERATSEFIKQILDGVNL 118
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 101 NPWVNIHVEYETSEEMITLVLETAAGGLSDQCVADRDAFNEKQRLMRQILLEGVFL 160
OY 119 HTKIAHFDLKPENIMLDKNDIPRIKILDEGLAHEIDGYEFKPIFTPTPEVAPVYN 178
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 161 HTHVAVHLDLKPQNILTSSES-PLGDIKIVDFGLSRIVKNSSELRIMQTPPEVAPV 219
OY 179 YEPLGLDMSIGVITVILLGSGAPLGDQKQETLANITSVSDPEEFHSHTSELANOF 238
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 220 YDPISMAIDMSIGVITVYMLTGISPLGDNKQETFLNISQMLSYSEEDFVSESADV 279
OY 239 FIRKLIVETRRKRLTIQALRHPMI 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 FIRKLIVKPPEDRAFDCECLKHPWL 304

RESULT 6
S17A_HUMAN STANDARD; PRT; 414 AA.
ID S17A_HUMAN
AC 09065: 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related
apoptosis-inducing protein kinase 1).
GN STK17A OR DRAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-90.
RC TISSUE=placenta, and liver;
RX MEDLINE=99003259; PubMed=9786912;
RA Sanjo H., Kawal T., Akira S.;
RA "DRAKs, novel serine/threonine kinases related to death-associated
protein kinase that trigger apoptosis."
RT J. Biol. Chem. 273:29066-29071(1998).
CC -1- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN
EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-
TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
INITIATION OF APOPTOSIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN LOWER
LEVELS IN HEART, LUNG, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
DR EMBL; AB011420; BAA34126.1; -
DR HSSP; P00518; IPRK.
DR MIM; 604726; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase: Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Nuclear protein; Apoptosis.
FT DOMAIN 61 321 PROTEIN KINASE.
FT NP_BIND 33 37 POLY-PRO.
FT BINDING 67 75 ATP (BY SIMILARITY).
FT BINDING 90 90 ATP (BY SIMILARITY).

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Db 750 HPKLVQCVDAFEEKANIVWLETVSGELFERIDFELFERECIKYMRQISEGVYIH 809
 QY 120 TKIAHFDLKPENIMLDKNIPPIHKLIDFGIAHEIEDGVCFKNIQFPEFAPEIVNY 179
 Db 810 KQGIIVHDLKRENIQVYKKT--GTRIKLIDFGIARLEKNGSLKYIFGPEFAPEIVNY 867
 QY 180 EPLGLEADMSIGVITYITLLSGASPLGDTKQETLANITSVSYDPEDEFFSHISELAKDF 239
 Db 868 EPISTATVMTMSIGVICYILVSGLSPLFGMDNETLANVTSATWDFDEAFDEISIDAKDF 927
 QY 240 IKRLVKEKTRKRLTIQEAALHPMI 263
 Db 928 ISNLLKDKMKRNLDTCTOCLQHPWL 951

RESULT 8
 ID 157B_HUMAN STANDARD; PRT: 372 AA.
 AC 094768;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Serine/threonine kinase 17b (EC 2.7.1.-) (DAP kinase-related
 apoptosis-inducing protein kinase 2).
 GN STR17b OR DRK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND MUTAGENESIS OF LYS-62.
 RC TISSUE=Placenta, and Liver;
 RX MEDLINE=99003259; PubMed=9786912;
 RA Sanjo H., Kawai T., Akira S.;
 RT "DRKs, novel serine/threonine kinases related to death-associated
 protein kinase that trigger apoptosis.";
 RL J. Biol. Chem. 273:29066-29071(1998).
 CC -1- FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN
 EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-
 TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
 INITIATION OF APOPTOSIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA, LUNG, PANCREAS
 AND IN LOWER LEVELS IN HEART, BRAIN, LIVER, SKELETAL MUSCLE AND
 KIDNEY.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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 or send an email to license@sib-sib.ch).
 CC EMBL: AB011421; BAA34127.1;
 CC HSSP: P00518; IPK.
 DR MIM: 604727;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation; Nuclear protein; Apoptosis.
 FT DOMAIN 33 293 PROTEIN KINASE.
 FT DOMAIN 308 311 POLY-SER.
 FT NP_BIND 39 47 ATP (BY SIMILARITY).

FT BINDING 62 62 ATP (BY SIMILARITY).
 FT MUTAGEN 62 62 K->A: LOSS OF ACTIVITY.
 SO SEQUENCE 372 AA; 42344 MW; 7E69FFAD6DC1FF3 CRC64;
 Query Match 46.5%; Score 625; DB 1; Length 372;
 Best Local Similarity 48.3%; Pred. No. 1-3e-33; Indels 10; Gaps 5;
 Matches 127; Conservative 46; Mismatches 80;
 QY 5 EELSGQPAIVKCKRKSGLEAYAKFIKRRSARRGVG--REIEEVSILKQVH-H 62
 Db 37 KELGRGFVAVRQCISKSTSGOEYAKFLKR-----RGGOCRAEILHEIVLILASCP 91
 QY 63 NVITLHDVYENRDVYHIELVSGELDFPLAK--ESLSEEAATSPKQILIDGVNLYLT 120
 Db 92 RVIMLHEVYENTSEILILEYVAGGEIFSLCPDLAEMVSENDVRLKQILEGVYVYHQ 151
 QY 121 KKAHFDLKPENIMLDKNIPPIHKLIDFGIAHEIEDGVCFKNIQFPEFAPEIVNYE 180
 Db 152 NNIVHDLKLPONT-LSSITPLGDIKIVDGMGRKIGHACEIREIMGPEYLAPELIND 210
 QY 181 PGLGLEADMSIGVITYITLLSGASPLGDTKQETLANITSVSYDPEDEFFSHISELAKDFI 240
 Db 211 PTTTMDVMNIGITAYMLTHTSPFVEDNQETVYLNISQVNDVSEPTFSSVQLATDFI 270
 QY 241 KRLVKEKTRKRLTIQEAALHPMI 263
 Db 271 QSLVKNPEKREPTAETICLSHML 293

RESULT 9
 ID KMTS_SHEEP STANDARD; PRT: 438 AA.
 AC 002827;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
 GN [Contains: Telokin] (Fragment).
 OS Myk.
 OC Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96139839; PubMed=8569750;
 RX Pato M.D., Kerc E., Lye S.J.;
 RA "Phosphorylation and partial sequence of pregnant sheep myometrium
 RT myosin light chain kinase.";
 RL Mol. Cell. Biochem. 149:59-65(1995).
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
 MYOSIN LIGHT CHAIN.
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
 light-chain] phosphate.
 CC -1- DOMAIN: TELOKIN BINDS CALMODULIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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 or send an email to license@sib-sib.ch).
 CC EMBL: S80867; AAB50715.2;
 DR HSSP: P56276; IYLK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.


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DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00047; 1g. 1.
DR SMART: SM00069; pkinase. 1.
DR SMART: SM00408; Igc2. 1.
DR SMART: SM00220; S_TKC. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; PARTIAL.
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN <1 241 PROTEIN KINASE.
FT DOMAIN 233 296 CALMODULIN-BINDING.
FT DOMAIN 346 413 IG-LIKE C2-TYPE DOMAIN.
FT BINDING 15 15 ATP (BY SIMILARITY).
FT ACT_SITE 107 107 BY SIMILARITY.
FT DOMAIN 283 438 TELOKIN.
FT DOMAIN 433 438 POLY-GLU.
SQ SEQUENCE 438 AA; 49503 MW; 77A02F485A10B51 CRC64;

Query Match 45.5%; Score 611.5; DB 1; Length 438;
Best Local Similarity 48.2%; Pred. No. 1.3e-32;
Matches 118; Conservative 46; Mismatches 72; Indels 9; Gaps 3;

OY 20 EKSTGLEVAKFIKKRQSRASRGVSREREVSILROYLHNHNVITLHDVYENRTDVH 79
DB 5 EKTGKVMKAFKFRANSK-----EKNTRQETISIMNCLHNPVLVCVAFKKATIVM 58
OY 80 ILELVSGELDFDLAOK- SLSEEAATSFQKILDGVNVLHTKKIAFDLKPENIMLDK 138
DB 59 VLEIVSGELFERIIDDFLTERECKYKMKQSEGEVYHKKGIYVLDLKPENIMKVNK 118
OY 139 NIPPIAKLIDFGLAHEIDEGVEFKNIFGTPREVAPEIVYEPDLGELADMSICVITYIL 198
DB 119 T-GTRKILDFGLARLEENAGSLKVLFGTPREVAPEIVYEPDLGELADMSICVITYIL 176
OY 199 LSGAPFLDGTQKQETLANITSVSDPEEFHSITSELAQFIRKLKTRKRLTIQDAL 258
DB 177 VSLSPFMGNDNETLANVTSATWDFDEAFDELSDAKQFISMLKKDKINRLCTOCL 236
OY 259 RHPWI 263
DB 237 QHPWL 241

RESULT 10
KMLC_RABIT STANDARD; PRT; 607 AA.
AC P07313;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase, skeletal muscle (BC 2.7.1.117) (MLCK).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=90110242; Pubmed=1688558;
RA Hering B.P., Stull J.T., Gallagher P.J.;
RT "Domain characterization of rabbit skeletal muscle myosin light chain
kinase."
RT J. Biol. Chem. 265:1724-1730(1990).
RN (2)
RN SEQUENCE OF 1-603.
RX MEDLINE=87101105; Pubmed=3542042;
RA Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;
RT "Amino acid sequence of rabbit skeletal muscle myosin light chain
kinase."
RN Biochemistry 25:8049-8057(1986).
RN (3)

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RP SEQUENCE OF 295-603.
RX MEDLINE=86104095; Pubmed=3841288;
RA Takio K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
RA Titani K.;
RT "Amino acid sequence of an active fragment of rabbit skeletal muscle
myosin light chain kinase."
RL Biochemistry 24:6028-6037(1985).
RN (4)
RP STRUCTURE BY NMR OF 577-602.
RX MEDLINE=92263094; Pubmed=1585175;
RA Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
RT "Solution structure of a calmodulin-target peptide complex by
multidimensional NMR."
RL Science 256:632-638(1992).
CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
MYOSIN LIGHT CHAIN.
CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
light-chain] phosphate.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
DR EMBL: J05194; AAA31400.1; -.
DR PIR: A25830; A25830.
DR PIR: A05120; A05120.
DR PIR: A35021; A35021.
DR PDB: 2BBM; 31-JAN-94.
DR PDB: 2BBN; 31-JAN-94.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Acetylation; 3D-structure.
FT INIT_MET 0
FT MOD_RES 1 1 ACETYLTATION.
FT DOMAIN 296 551 PROTEIN KINASE.
FT DOMAIN 585 597 CALMODULIN-BINDING.
FT NP_BIND 302 310 ATP (BY SIMILARITY).
FT BINDING 325 325 ATP (BY SIMILARITY).
FT ACT_SITE 417 417 BY SIMILARITY.
FT CONFLICT 335 335 K -> KK (IN REF. 2 AND 3).
FT HELIX 581 595
FT TURN 596 596
SQ SEQUENCE 607 AA; 65337 MW; 6E677641751A04C8 CRC64;

Query Match 42.6%; Score 571.5; DB 1; Length 607;
Best Local Similarity 43.1%; Pred. No. 6.9e-30;
Matches 112; Conservative 54; Mismatches 85; Indels 9; Gaps 3;

OY 5 EELSGGFAYKKCKREKSTGLEVAKFIKKRQSRASRGVSREREVSILROYLHNHNV 64
DB 300 EALGGGKFGAVCTETKSTGKLAKAYKKQTPK-----DKENVMLEIEVMNOLNHRNL 353
OY 65 ITLHDVYENRTDVHIIELVSGELDFDLAOK- SLSEEAATSFQKILDGVNVLHTKKI 123
DB 354 IQLVAAIETPREHIVLEVMYIEGGELEFRIYVDYHLEFVDMVVRQCDGILFHHKRV 413
OY 124 AHPDLKPEINMLDKNIPPIAKLIDFGLAHEIDEGVEFKNIFGTPREVAPEIVYEPDLG 183
DB 414 LHLDKPEINILCVMTTGH--VKIIDFGLARYNPENKLVNFTPEFLSPVAVNYDQIS 471
OY 184 LEADMSIGVITYILLSGASPLDGTQKQETLANITSVSDPEEFHSITSELAQFIRKL 243

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Db 472 DKTDMWSLGVITVYMLLSGLSPFLGDDDETETLNNVLNSGWFDEETFEAVSDEAKDFVSNL 531
QY 244 LKETERKRLTIOEALRHPMI 263
Db 532 LKQEGARMSAEOCLAHPML 551

RESULT 11
KMLC_RAT
ID KMLC_RAT STANDARD: PRT: 609 AA.
AC P20689;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=88273159; PubMed=2839493;
RX Roush C.L., Kennelly P.J., Giaccum M.B., Helfman D.M., Scott J.D.,
RA Krebs E.G.;
RT "Isolation of the cDNA encoding rat skeletal muscle myosin light
RL chain kinase. Sequence and tissue distribution.";
CC J. Biol. Chem. 263:10510-10516(1988).
CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC MYOSIN LIGHT CHAIN.
CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC light-chain] phosphate.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
CC EMBL: J03886; AAA1625.1; ALT_SEQ.
CC PIR: A28798; A28798.
CC HSSP: P00518; 1PKK.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC TRANSFASER: Serine/threonine-protein kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Acetylation.
KW INIT_MET 0
KW MOD_RES 1
FT DOMAIN 298 553 ACETYLATION (BY SIMILARITY).
FT DOMAIN 587 599 CALMODULIN-BINDING (BY SIMILARITY).
FT NP_BIND 304 312 ATP (BY SIMILARITY).
FT BINDING 327 327 ATP (BY SIMILARITY).
FT ACT_SITE 419 419 BY SIMILARITY.
SQ SEQUENCE 609 AA; 65685 MW; 0073A22659BD1358 CRC64;

Query Match 42.5%; Score 570.5; DB 1; Length 609;
Best Local Similarity 41.5%; Pred. No. 8e-30; Indels 9; Gaps 3;
Matches 108; Conservative 58; Mismatches 85;

QY 5 EELSGGQRAIYKKCKEKSTGEVYAKFTKRSRSGVSRERIEVSILROVLAHNY 64
Db 302 EALGGGKFGAVCTCTERSTGLAKAVIKKOTPK-----DKEMVLLIEVMQNLNRNL 355
QY 65 IFLADVENVKTDVHILELVSGGELDFLAQK-SLSEELATSTIKQILDGQVNVLHKKI 123

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Db 356 IOIYSAIETSHHILFMNYIEGGELFERIVEDQOLTEVDMVFRQICGILFMHMKRV 415
QY 124 AHFDLKPENIMLLDKNPIPIPHKILDFCLAHIEDGVFEKNIPTGPFEVAFIYNEPLG 183
Db 416 LHLDLKPEINILCVNFTGHL--VKIIDFGLARRYNENKATKFNFGPELSEVANNYDIS 473
QY 184 LEADMSIGVITYIILSGASPFGLDGTQETLANITSVSYDFDEEFSHTSELANDFIKLL 243
Db 474 DKTDMWSLGVITVYMLLSGLSPFLGDDDETETLNNVLNSGWFDEETFEAVSDEAKDFVSNL 533
QY 244 LKETERKRLTIOEALRHPMI 263
Db 534 ITRQSGARMSAEOCLAHPML 553

RESULT 12
KMLC_DICDI
ID KMLC_DICDI STANDARD: PRT: 295 AA.
AC P25323;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain kinase (EC 2.7.1.117) (MLCK).
DE MYOSELINUM DISCOIDEUM (Slime mold).
OS Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OC NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AX3;
RX MEDLINE=91340753; PubMed=1651931;
RA Tan J.L., Spudich J.A.;
RT "Characterization and bacterial expression of the dictyostelium
RL domain.";
RT J. Biol. Chem. 266:16044-16049(1991).
RN [2]
RP REVISIONS.
RA Spudich J.A.;
RA Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE.
RX STRAIN=AX3;
RX MEDLINE=90337997; PubMed=2380188;
RA Tan J.L., Spudich J.A.;
RT "Dictyostelium myosin light chain kinase. Purification and
RT characterization.";
RL J. Biol. Chem. 265:13818-13824(1990).
CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC MYOSIN LIGHT CHAIN.
CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC light-chain] phosphate.
CC -1- ENZYME REGULATION: POSSESSES AN AUTONHIBITORY DOMAIN.
CC AUTOPHOSPHORYLATION APPEARS TO INCREASE THE ENZYMIC ACTIVITY.
CC DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M64176; AAB06337.1; -.
CC PIR: A40811; A40811.
CC PIR: A37125; A37125.
CC HSSP: 063450; 1A06.
CC DictyDB: DD01034; mlka.
CC InterPro: IPR000719; Euk_pkinase.

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DR	EMBL: M64757; AAAA0835.1; -	
DR	EMBL: M64757; AAAA0857.1; -	
DR	EMBL: J04600; AAAA1867.1; -	
DR	EMBL: J04446; AAAA0990.1; -	
DR	PIR: A11103; TVRRC4.	
DR	HSSP; P00518; IPHK.	
DR	InterPro; IPR000719; Euk_PKinase.	
DR	InterPro; IPR002290; Ser_lhr_kinase.	
DR	InterPro; IPR00069; PKinase; 1.	
DR	SMART; SM00220; S_TKc; 1.	
DR	SMART; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
KM	Transferrase: Serine/threonine-protein Kinase; ATP-binding; Calmodulin-binding; Testis; Alternative splicing; CALSPERMIN.	
KM	CHAIN	306 474
FT	DOMAIN	42 296
FT	NP_BIND	48 56
FT	BINDING	71 71
FT	ACT_SITE	160 160
FT	DOMAIN	318 357
FT	DOMAIN	393 399
FT	DOMAIN	403 413
FT	CONFLICT	372 372
FT	CONFLICT	I -> M (IN REF. 2 AND 4).
FT	SEQUENCE	474 AA; 55133 MW; 56F71AC5644DEB23 CRC64;

Query Match	37.7%	Score 506	DB 1	Length 474
Best Local Similarity	40.3%	Pred. No. 8.5e-26		
Matches 108	Conservative 50	Mismatches 92	Indels 18	Gaps
QY	1	YDGEELGSGGFAIVKCKREKSTGLEVAFAKFIKKROSRSARKVSRREITREYSIIIRQVL	60	
Db	42	FEVSEELGRGRTSTIVYCKGCKGTQKPYALALVKTKT-----VDKIVTFETGVLLRS	93	
QY	61	HHNVITLHDVYENKTDVHHILEVSGGELDFEFLAOKESLSEEAATSPFIKOLIDGVNYLHT	120	
Db	94	HPNIIKKEIETPELSTLVLELTGGEELPRIVYKGYTSERDAADAVKOLLEAVAYLH	153	
QY	121	KKIAHFEDKPENIMLDKNIPH--IKLIDFGLAHELDGCEFFKNEGPPEFVAPETVN	178	
Db	154	NCIVAROLKPEMLLYA--TPAPAPLKIADFGISKIEHOVLKMYCGTGYCAPELLR	210	
QY	179	VEPLGLEDMMSIGVITYILLSGASPEL---GDTKQETLANITSVSYDFDEFFSHSEL	235	
Db	211	GCAYGPEVDMSVGLITTYILLGPEFFDERGD--QFMFRILNCEYFISPMWDEVSLN	268	
QY	236	AKDFIRKLKLVETRRKRLTIQELALRPWT	263	
Db	269	AKDLVKKLIVLDPKRRKLTTFQALQHPW	296	
RESULT 15				
KCCA_MOUSE	STANDARD	PRT	469 AA.	
AC	P08414	G61381		
AD	01-AUG-1988	(Rel. 08, Created)		
AT	01-APR-1993	(Rel. 25, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	calcium/calmodulin-dependent protein kinase type IV catalytic chain			
DE	(EC 2.7.1.123) (CAM kinase-GR) (CaMK IV) [Contains: Calypterin]			
GN	CaMK4			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C; TISSUE-Brain;			
RA	MEDLINE=91372388; PubMed=1893997;			
RT	Jones D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;			
RT	"cDNA sequence and differential expression of the mouse			
RT	Ca2+/calmodulin-dependent protein kinase IV gene."			

RL FEBS Lett. 289:105-109(1991).
 RN [2]
 RP SEQUENCE OF 240-469 FROM N.A.
 RX MEDLINE-89122027; PubMed-2536634;
 RA Sikeja J.M., Law M.L., Kao F.-T., Hartz J.A., Wei Q., Hahn W.E.;
 RT "Chromosomal localization of the human gene for brain
 Ca2+/calmodulin-dependent protein kinase type IV.";
 RL Genomics 4:21-27(1989).
 RN [3]
 RP SEQUENCE OF 315-469 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-87204263; PubMed-3033675;
 RA Sikeja J.M., Hahn W.E.;
 RT "Screening an expression library with a ligand probe: isolation and
 RT sequence of a cDNA corresponding to a brain calmodulin-binding
 RT protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042(1987).
 CC -/- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
 CC PROTEIN.
 CC -/- CATALYTIC ACTIVITY: ATP + protein - ADP + O-phosphoprotein.
 CC -/- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
 CC NUCLEI.
 CC -/- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
 CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
 CC SPLICING.
 CC -/- TISSUE SPECIFICITY: BRAIN AND TESTIS.
 CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.

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 DR EMBL: M16206; AAA39933.1; -;
 DR EMBL: M64266; AAA37364.1; -;
 DR EMBL: J03057; AAA37366.1; -;
 DR EMBL: X58995; CAA41741.1; -;
 DR PIR: A29878; A29878.
 DR PIR: S17656; S17656.
 DR HSSP: 063450; 1A06.
 DR MGD: MGI:88258; Camk4.
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: PF00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Calmodulin-binding; alternative splicing.
 KW CHAIN 306 469
 FT DOMAIN 42 296 CALSPERMIN.
 FT NP_BIND 48 56 PROTEIN KINASE.
 FT BINDING 71 71 ATP (BY SIMILARITY).
 FT ACT_SITE 160 160 ATP (BY SIMILARITY).
 FT DOMAIN 318 337 BY SIMILARITY.
 FT DOMAIN 278 280 CALMODULIN-BINDING (POTENTIAL).
 FT CONFLICT 278 280 VLD -> CREGI (IN REF. 2).
 FT CONFLICT 302 302 N -> T (IN REF. 2).
 SO SEQUENCE 469 AA; 52627 MW; 52627 MW; CEIP98670822F975 CRC64;

Query Match 37.6%; Score 505; DB 1; Length 469;
 Best Local Similarity 40.3%; Pred. No. 9,7e-26;
 Matches 108; Conservative 50; Mismatches 92; Indels 18; Gaps 5;
 QY 1 YDIGEELGSGQFAIVKCKREKSTGLEIAKFIKKRSGASRGVSRREIEREVSILRQVL 60
 DB 42 FEVESEELGSGATSIYVRCOKGTOKGPYALKVLKKT-----VDKRIVTEIGVLLRLS 93

QY 61 HNAVITLADVYENRTDVVHILEYSGGELFDPLAQKESLSEEAATSFIRKOLLGVNLYHT 120
 DB 94 HPIIKIKLEIFETPTETLSIVLELYTGGEIDRIVEKGYTSRQDARDAVKOLLEAVAILHE 153
 QY 121 KKAHFDLKPENIMLLDKNIPIPH--IKLIDFGLAHEIDGVEFKNIFGPEFYAPEIVN 178
 DB 154 NGIVHRLDKPENLLYA--TPAPDAPKIIDFGISLIVEHQVLKFTVCGTFPGYCAPETLR 210
 QY 179 YEPGLADWMSIGVITYIILSGASPL---GDTKQETLANITSVSYDFDEEFFSHTSSEL 235
 DB 211 GCAYGPEVDMWSVGIITYIILCGEPPEYDERGD--QEFRRILNCEYFFISPMWDEVSLN 268
 QY 236 AKDFIRKLIVKETRRRLTIOEALRHPWI 263
 DB 269 AKDLVKKLIYDPPKRLITTFQALQHPNV 296

Search completed: May 18, 2002, 05:12:37
 Job time: 1438 sec

Sat May 18 15:09:11 2002

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